

SEQUENCE LISTING

<110> Garvan Institute of Medical Research

<120> Method of modulating bone growth, remodeling and adiposity

<130> 42-000400US

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1180

<212> DNA

<213> human neuropeptide Y1 receptor

<220>

<221> CDS

<222> (7)..(1161)

<400> 1

aagctt	atg	aat	tca	aca	tta	ttt	tcc	cag	gtt	gaa	aat	cat	tca	gtc	48	
	Met	Asn	Ser	Thr	Leu	Phe	Ser	Gln	Val	Glu	Asn	His	Ser	Val		
1					5					10						
cac	tct	aat	ttc	tca	gag	aag	aat	gcc	cag	ctt	ctg	gct	ttt	gaa	aat	96
His	Ser	Asn	Phe	Ser	Glu	Lys	Asn	Ala	Gln	Leu	Leu	Ala	Phe	Glu	Asn	
15					20					25				30		
gat	gat	tgt	cat	ctg	ccc	ttg	gcc	atg	ata	ttt	acc	tta	gct	ctt	gct	144
Asp	Asp	Cys	His	Leu	Pro	Leu	Ala	Met	Ile	Phe	Thr	Leu	Ala	Leu	Ala	
				35					40					45		
tat	gga	gct	gtg	atc	att	ctt	ggt	gtc	tct	gga	aac	ctg	gcc	ttg	atc	192
Tyr	Gly	Ala	Val	Ile	Ile	Leu	Gly	Val	Ser	Gly	Asn	Leu	Ala	Leu	Ile	
			50					55					60			
ata	atc	atc	ttg	aaa	caa	aag	gag	atg	aga	aat	gtt	acc	aac	atc	ctg	240
Ile	Ile	Ile	Leu	Lys	Gln	Lys	Glu	Met	Arg	Asn	Val	Thr	Asn	Ile	Leu	
			65				70					75				
att	gtg	aac	ctt	tcc	ttc	tca	gac	ttg	ctt	gtt	gcc	atc	atg	tgt	ctc	288
Ile	Val	Asn	Leu	Ser	Phe	Ser	Asp	Leu	Leu	Val	Ala	Ile	Met	Cys	Leu	
	80					85					90					
ccc	ttt	aca	ttt	gtc	tac	aca	tta	atg	gac	cac	tgg	gtc	ttt	ggt	gag	336
Pro	Phe	Thr	Phe	Val	Tyr	Thr	Leu	Met	Asp	His	Trp	Val	Phe	Gly	Glu	
95					100					105				110		
gcg	atg	tgt	aag	ttg	aat	cct	ttt	gtg	caa	tgt	gtt	tca	atc	act	gtg	384
Ala	Met	Cys	Lys	Leu	Asn	Pro	Phe	Val	Gln	Cys	Val	Ser	Ile	Thr	Val	
				115					120					125		
tcc	att	ttc	tct	ctg	gtt	ctc	att	gct	gtg	gaa	cga	cat	cag	ctg	ata	432
Ser	Ile	Phe	Ser	Leu	Val	Leu	Ile	Ala	Val	Glu	Arg	His	Gln	Leu	Ile	
			130					135					140			
atc	aac	cct	cga	ggg	tgg	aga	cca	aat	aat	aga	cat	gct	tat	gta	ggg	480

Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly	
145 150 155	
att gct gtg att tgg gtc ctt gct gtg gct tct tct ttg cct ttc ctg	528
Ile Ala Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu	
160 165 170	
atc tac caa gta atg act gat gag ccg ttc caa aat gta aca ctt gat	576
Ile Tyr Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp	
175 180 185 190	
gcg tac aaa gac aaa tac gtg tgc ttt gat caa ttt cca tcg gac tct	624
Ala Tyr Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser	
195 200 205	
cat agg ttg tct tat acc act ctc ctc ttg gtg ctg cag tat ttt ggt	672
His Arg Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly	
210 215 220	
cca ctt tgt ttt ata ttt att tgc tac ttc aag ata tat ata cgc cta	720
Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu	
225 230 235	
aaa agg aga aac aac atg atg gac aag atg aga gac aat aag tac agg	768
Lys Arg Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg	
240 245 250	
tcc agt gaa acc aaa aga atc aat atc atg ctg ctc tcc att gtg gta	816
Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val	
255 260 265 270	
gca ttt gca gtc tgc tgg ctc cct ctt acc atc ttt aac act gtg ttt	864
Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe	
275 280 285	
gat tgg aat cat cag atc att gct acc tgc aac cac aat ctg tta ttc	912
Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe	
290 295 300	
ctg ctc tgc cac ctc aca gca atg ata tcc act tgt gtc aac ccc ata	960
Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile	
305 310 315	
ttt tat ggg ttc ctg aac aaa aac ttc cag aga gac ttg cag ttc ttc	1008
Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe	
320 325 330	
ttc aac ttt tgt gat ttc cgg tct cgg gat gat gat tat gaa aca ata	1056
Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile	
335 340 345 350	
gcc atg tcc acg atg cac aca gat gtt tcc aaa act tct ttg aag caa	1104
Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln	
355 360 365	
gca agc cca gtc gca ttt aaa aaa atc aac aac aat gat gat aat gaa	1152
Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu	
370 375 380	
aaa atc tga aactacttat agctctaga	1180

Lys Ile

<210> 2
<211> 384
<212> PRT
<213> human neuropeptide Y1 receptor

<400> 2

Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser
1 5 10 15

Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp
20 25 30

Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
35 40 45

Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
50 55 60

Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
65 70 75 80

Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
85 90 95

Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
100 105 110

Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
115 120 125

Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
130 135 140

Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
145 150 155 160

Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
165 170 175

Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
180 185 190

Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
Page 3

195

200

205

Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
 210 215 220

Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
 225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
 245 250 255

Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
 260 265 270

Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
 275 280 285

Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
 290 295 300

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
 305 310 315 320

Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
 325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
 340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
 355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
 370 375 380

<210> 3

<211> 3747

<212> DNA

<213> human neuropeptide Y2 receptor

<220>

<221> CDS

<222> (496)..(1638)

<400> 3

gaattcggcc gctgagagac cctggacact gttcctgctc cctcgccacc aaaacttctc

60

ctccagtc	ctccctgca	ggaccatcgc	ccgcagcctc	tgcacctgtt	ttcttgtgtt	120
taaggggtggg	gtttgcccc	ctccccacgc	tcccatctct	gatcctccca	ccttcacccg	180
cccacccccgc	gagtgagtgc	ggtgcccagg	cgcgcttggc	ctgagagggtc	ggcagcagac	240
ccggcagcgc	caaccgcccc	gccgctctga	ctgctccggc	tgcccgcccc	cgcggcgcgcg	300
gctgtcctgg	accctaggag	gggacggaac	cggacttgcc	tttgggcacc	ttccagggcc	360
ctctccaggt	cggctggcta	atcatcggac	agacggactg	cacacatctt	gtttccgcgt	420
ctccgcaaaa	acgcgagggtc	caggtcagtt	gtagactctt	gtgctggttg	caggccaagt	480
ggacctgtac	tgaaa	atg ggt cca ata	ggt gca gag gct	gat gag aac cag		531
		Met Gly Pro Ile	Gly Ala Glu Ala	Asp Glu Asn Gln		
		1	5	10		
aca gtg gaa gaa	atg aag gtg gaa	caa tac ggg cca	caa aca act cct			579
Thr Val Glu Glu	Met Lys Val Glu	Gln Tyr Gly Pro	Gln Thr Thr Pro			
	15	20	25			
aga ggt gaa ctg	gtc cct gac cct	gag cca gag ctt	ata gat agt acc			627
Arg Gly Glu Leu	Val Pro Asp Pro	Glu Pro Glu Leu	Ile Asp Ser Thr			
	30	35	40			
aag ctg att gag	gta caa gtt gtt	ctc ata ttg gcc	tac tgc tcc atc			675
Lys Leu Ile Glu	Val Gln Val Val	Leu Ile Leu Ala	Tyr Cys Ser Ile			
	45	50	55			60
atc ttg ctt ggg	gta att ggc aac	tcc ttg gtg atc	cat gtg gtg atc			723
Ile Leu Leu Gly	Val Ile Gly Asn	Ser Leu Val Ile	His Val Val Ile			
	65	70	75			
aaa ttc aag agc	atg cgc aca gta	acc aac ttt ttc	att gcc aat ctg			771
Lys Phe Lys Ser	Met Arg Thr Val	Thr Asn Phe Phe	Ile Ala Asn Leu			
	80	85	90			
gct gtg gca gat	ctt ttg gtg aac	act ctg tgt cta	ccg ttc act ctt			819
Ala Val Ala Asp	Leu Leu Val Asn	Thr Leu Cys Leu	Pro Phe Thr Leu			
	95	100	105			
acc tat acc tta	atg ggg gag tgg	aaa atg ggt cct	gtc ctg tgc cac			867
Thr Tyr Thr Leu	Met Gly Glu Trp	Lys Met Gly Pro	Val Leu Cys His			
	110	115	120			
ctg gtg ccc tat	gcc cag ggc ctg	gca gta caa gta	tcc aca atc acc			915
Leu Val Pro Tyr	Ala Gln Gly Leu	Ala Val Gln Val	Ser Thr Ile Thr			
	125	130	135			140
ttg aca gta att	gcc ctg gac cgg	cac agg tgc atc	gtc tac cac cta			963
Leu Thr Val Ile	Ala Leu Asp Arg	His Arg Cys Ile	Val Tyr His Leu			
	145	150	155			
gag agc aag atc	tcc aag cga atc	agc ttc ctg att	att ggc ttg gcc			1011
Glu Ser Lys Ile	Ser Lys Arg Ile	Ser Phe Leu Ile	Ile Gly Leu Ala			
	160	165	170			
tgg ggc atc agt	gcc ctg ctg gca	agt ccc ctg gcc	atc ttc cgg gag			1059
Trp Gly Ile Ser	Ala Leu Leu Ala	Ser Pro Leu Ala	Ile Phe Arg Glu			

175	180	185	
tat tcg ctg att gag atc att ccg gac ttt gag att gtg gcc tgt act			1107
Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr			
190	195	200	
gaa aag tgg cct ggc gag gag aag agc atc tat ggc act gtc tat agt			1155
Glu Lys Trp Pro Gly Glu Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser			
205	210	215	220
ctt tct tcc ttg ttg atc ttg tat gtt ttg cct ctg ggc att ata tca			1203
Leu Ser Ser Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser			
	225	230	235
ttt tcc tac act cgc att tgg agt aaa ttg aag aac cat gtc agt cct			1251
Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro			
	240	245	250
gga gct gca aat gac cac tac cat cag cga agg caa aaa acc acc aaa			1299
Gly Ala Ala Asn Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys			
	255	260	265
atg ctg gtg tgt gtg gtg gtg gtg ttt gcg gtc agc tgg ctg cct ctc			1347
Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu			
	270	275	280
cat gcc ttc cag ctt gcc gtt gac att gac agc cag gtc ctg gac ctg			1395
His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu			
	285	290	300
aag gag tac aaa ctc atc ttc aca gtg ttc cac att atc gcc atg tgc			1443
Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys			
	305	310	315
tcc act ttt gcc aat ccc ctt ctc tat ggc tgg atg aac agc aac tac			1491
Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr			
	320	325	330
aga aag gct ttc ctc tcg gcc ttc cgc tgt gag cag cgg ttg gat gcc			1539
Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala			
	335	340	345
att cac tct gag gtg tcc gtg aca ttc aag gct aaa aag aac ctg gag			1587
Ile His Ser Glu Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu			
	350	355	360
gtc aga aag aac agt ggc ccc aat gac tct ttc aca gag gct acc aat			1635
Val Arg Lys Asn Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn			
	365	370	380
gtc taaggaagct gtggtgtgaa aatgtatgga tgaattctga ccagagctat			1688
Val			
gaatctgggt gatggcggct cacaagtgaa aactgatttc ccattttaaa gaagaagtgg			1748
atctaaatgg aagcatctgc tgtttaattc ctggaaaact ggctgggcag agcctgtgtg			1808
aaaatactgg aattcaaaga taaggcaaca aaatgggttta cttaacagtt ggttgggtag			1868

taggttgc	at	gagtaaa	agcagagaga	agtactttt	g	attat	tttcc	tg	gagtgaag	1928			
aaaacttg	aa	caagaaatt	gtattatcaa	agcattgct	g	agagacgg	tg	gg	aaaaataag	1988			
ttgacttt	ca	aatcacgt	ta	ggacctgg	at	tgaggagg	tg	tcagttcgc	tgctccctgc	2048			
ttggcttat	g	aaaacacc	ac	tgaacagaaa	tttctccag	g	agccacag	g	ctctccttca	2108			
tcgcatttt	g	at	ttttttt	gt	tcattctcta	g	acaaaaatcc	atcaggg	aat	gctgcaggaa	2168		
acgattgcca	actatacg	aa	tg	gcttcgag	gagataaa	act	gaaat	tttgct	atataa	attaa	2228		
tat	tttggca	gatgatagg	g	aa	ctcctca	ac	actcag	tg	ggccaatt	gt	tcttaaaacc	2288	
aattgcac	gt	ttgg	tgaag	tttcttca	ac	tctgaat	caa	aagctg	aa	at	tctcagaatt	2348	
acaggaaa	atg	caaaccat	ca	tttaattt	ct	aatttca	agt	tacatcc	gct	ttatgg	agat	2408	
actat	tttaga	taacaaga	at	acaactt	gat	actttt	attg	ttatac	cttt	ttgaac	atgt	2468	
atgatt	ttctg	ttgttatt	cc	tattgg	agct	aagttt	gtct	acactaaa	at	ttaaat	caga	2528	
ctagaga	ata	at	ttttt	gtg	catgtt	gtaa	catttcac	ag	tatttaca	ag	ctat	tttttgc	2588
acagg	tacat	agctctc	atg	tattttaa	aga	acactgc	agt	gttatt	tttct	ttgaa	attca	2648	
tcctccac	gg	acccatt	cat	actaaata	aaa	acaatg	ta	at	tacattaaa	tg	gacctatc	2708	
tgtaag	aggt	actaaaaa	aca	ctggatt	cat	ttcatc	ttgc	aaatgt	tgt	tttcaa	acca	2768	
gtttcac	ata	agttatt	tgt	cttctttt	ca	aaataatt	ag	ctata	ttttt	atataat	atg	2828	
aatata	taca	taaaaa	attgt	ttctata	aat	tgtaga	acat	agatg	ctaca	gtatt	ttttta	2888	
tttaatt	tata	ttatga	ataa	aattgt	tatt	tcaatag	tac	ccaacca	aag	atgctt	aaaa	2948	
accttct	atg	ttcata	aaaaa	ataaca	actg	agatgt	taaa	atagtc	atac	gtcttt	tagat	3008	
gctatt	aaag	tttcatt	tagt	catatt	ttttg	taaat	atgac	agaatt	ttgtg	aatata	tttt	3068	
taaagc	aaaa	aacttca	aca	tgcat	atgat	atatag	ttac	aacatta	aatt	ttatga	actg	3128	
gagagc	ttta	ctttgt	ggat	atattt	aaaa	ttcat	attat	agctc	ctatt	aaattc	cttc	3188	
catgat	atagat	ataaagg	act	ggtttt	taag	tg	actgcac	ttctg	gaata	ctgaaa	aaga	3248	
atgaaa	acaa	tatgtt	tagat	taggt	gtaag	acttta	agaa	gcgaac	aaaa	agta	atgtat	3308	
atctg	taata	tataat	caaa	tgattc	at	ttctg	ttaga	ctagg	caa	at	tg	ttcaaaaa	3368
taacct	tttt	gtcttt	taag	tagcag	tcac	tttgct	taag	atgct	aatag	aaaact	gtgg	3428	
ttaaag	at	accctcc	ctc	ttgg	tgaatt	attac	actgt	aagaa	atgta	tatg	ctactg	3488	
tgttac	atgt	tgtatt	tagta	aattatt	aga	atcca	attaa	tgatt	caatt	aacata	tatc	3548	
ttatcca	aatt	cattat	gtca	attcatt	aat	aaaata	cctt	ttatg	tagag	gcttt	atgtt	3608	
gcaatt	aaaa	agttggg	aaa	atgaaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	3668	

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3728

aaaaaaaaa aaaaaaaaaa 3747

<210> 4

<211> 381

<212> PRT

<213> human neuropeptide Y2 receptor

<400> 4

Met Gly Pro Ile Gly Ala Glu Ala Asp Glu Asn Gln Thr Val Glu Glu
1 5 10 15

Met Lys Val Glu Gln Tyr Gly Pro Gln Thr Thr Pro Arg Gly Glu Leu
20 25 30

Val Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr Lys Leu Ile Glu
35 40 45

Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile Ile Leu Leu Gly
50 55 60

Val Ile Gly Asn Ser Leu Val Ile His Val Val Ile Lys Phe Lys Ser
65 70 75 80

Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu Ala Val Ala Asp
85 90 95

Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu Thr Tyr Thr Leu
100 105 110

Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His Leu Val Pro Tyr
115 120 125

Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr Leu Thr Val Ile
130 135 140

Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu Glu Ser Lys Ile
145 150 155 160

Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala Trp Gly Ile Ser
165 170 175

Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu Tyr Ser Leu Ile
180 185 190

Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr Glu Lys Trp Pro
195 200 205

Gly Glu Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser Leu Ser Ser Leu
210 215 220

Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser Phe Ser Tyr Thr
225 230 235 240

Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro Gly Ala Ala Asn
245 250 255

Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys Met Leu Val Cys
260 265 270

Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu His Ala Phe Gln
275 280 285

Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu Lys Glu Tyr Lys
290 295 300

Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys Ser Thr Phe Ala
305 310 315 320

Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe
325 330 335

Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala Ile His Ser Glu
340 345 350

Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu Val Arg Lys Asn
355 360 365

Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn Val
370 375 380

<210> 5
<211> 2260
<212> DNA
<213> human neuropeptide Y4 receptor

<220>
<221> CDS
<222> (660)..(1787)

<400> 5
ggatccccga ggcttttagct ctatcttgaa gggaaatgggg tgccgtggaa ggacacaagc

60

aatcctgtgc tgagtggcat ttattgctgt ctccattcag ataaaatgtg acaaggggca	120
ttctacccat gttccctgaa caattccgtc actaaagtct gcatacagca ctccaacttt	180
tttatcatca gaacagcctc atcctgagggc ggaggggaatt agtagaaciaa gttctggcat	240
tagatgacct gagtttgtaa ctgggcctgt tactaattag ctgtgtgact atgggcaagt	300
tgctttccat ctcaggggtct tagattcctc atctatgaaa cggattgata atatctacct	360
ctaggaataa actagctaata agacgaaaagt gctgagcaca gtaccagca tgcaacaagt	420
gcttctaaca aggtagcaat cattggatgc caatgtctca ccatgagcct taggtaatag	480
ccctccagat accagccttg ggttgaagc agctgagagc ctttctaccc ggccctgctc	540
ctctctggat tctaccctgg gcatgatccc tgagtattgt ttgtctgttt gccttgtagg	600
gcgtcatccc tcaagtgtat cacttagttc aagagtcctg gaatcttttc acatccact	659
atg aac acc tct cac ctc ctg gcc ttg ctg ctc cca aaa tct cca caa	707
Met Asn Thr Ser His Leu Leu Ala Leu Leu Leu Pro Lys Ser Pro Gln	
1 5 10 15	
ggt gaa aac aga agc aaa ccc ctg ggc acc cca tac aac ttc tct gaa	755
Gly Glu Asn Arg Ser Lys Pro Leu Gly Thr Pro Tyr Asn Phe Ser Glu	
20 25 30	
cat tgc cag gat tcc gtg gac gtg atg gtc ttc atc gtc act tcc tac	803
His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr	
35 40 45	
agc att gag act gtc gtg ggg gtc ctg ggt aac ctc tgc ctg atg tgt	851
Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys	
50 55 60	
gtg act gtg agg cag aag gag aaa gcc aac gtg acc aac ctg ctt atc	899
Val Thr Val Arg Gln Lys Glu Lys Ala Asn Val Thr Asn Leu Leu Ile	
65 70 75 80	
gcc aac ctg gcc ttc tct gac ttc ctc atg tgc ctc ctc tgc cag ccg	947
Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Leu Cys Gln Pro	
85 90 95	
ctg acc gcc gtc tac acc atc atg gac tac tgg atc ttt gga gag acc	995
Leu Thr Ala Val Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Thr	
100 105 110	
ctc tgc aag atg tcg gcc ttc atc cag tgc atg tcg gtg acg gtc tcc	1043
Leu Cys Lys Met Ser Ala Phe Ile Gln Cys Met Ser Val Thr Val Ser	
115 120 125	
atc ctc tcg ctc gtc ctc gtg gcc ctg gag agg cat cag ctc atc atc	1091
Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile	
130 135 140	
aac cca aca ggc tgg aag ccc agc atc tca cag gcc tac ctg ggg att	1139
Asn Pro Thr Gly Trp Lys Pro Ser Ile Ser Gln Ala Tyr Leu Gly Ile	
145 150 155 160	

gtg ctc atc tgg gtc att gcc tgt gtc ctc tcc ctg ccc ttc ctg gcc Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala 165 170 175	1187
aac agc atc ctg gag aat gtc ttc cac aag aac cac tcc aag gct ctg Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu 180 185 190	1235
gag ttc ctg gca gat aag gtg gtc tgt acc gag tcc tgg cca ctg gct Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala 195 200 205	1283
cac cac cgc acc atc tac acc acc ttc ctg ctc ctc ttc cag tac tgc His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys 210 215 220	1331
ctc cca ctg ggc ttc atc ctg gtc tgt tat gca cgc atc tac cgg cgc Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg 225 230 235 240	1379
ctg cag agg cag ggg cgc gtg ttt cac aag ggc acc tac agc ttg cga Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg 245 250 255	1427
gct ggg cac atg aag cag gtc aat gtg gtg ctg gtg gtg atg gtg gtg Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val 260 265 270	1475
gcc ttt gcc gtg ctc tgg ctg cct ctg cat gtg ttc aac agc ctg gaa Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu 275 280 285	1523
gac tgg cac cat gag gcc atc ccc atc tgc cac ggg aac ctc atc ttc Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe 290 295 300	1571
tta gtg tgc cac ttg ctt gcc atg gcc tcc acc tgc gtc aac cca ttc Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe 305 310 315 320	1619
atc tat ggc ttt ctc aac acc aac ttc aag aag gag atc aag gcc ctg Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu 325 330 335	1667
gtg ctg act tgc cag cag agc gcc ccc ctg gag gag tcg gag cat ctg Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu 340 345 350	1715
ccc ctg tcc aca gta cat acg gaa gtc tcc aaa ggg tcc ctg agg cta Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu 355 360 365	1763
agt ggc agg tcc aat ccc att taa ccaggtctag gtcttctccc tgccatgtcc Ser Gly Arg Ser Asn Pro Ile 370 375	1817
cttgccaggc tcttccactt agctaagtgg gcacactgca agctgggggtg gcaccccagc	1877
attcctggct ttctggggtc cagataggct ggcaagagct gtttttgcatt ccatttgcatt	1937

cgtgaagact ggcattttga tacttcagct gtttgttcct gggagaattc tgagcacaga 1997
 ttccagaggt cacagtaagc cttgcagctt gagctgaaag atgccagagc cggagatgtc 2057
 tgctggcagc aggcagggtt cattctgggtg acacagcaac agatccctgg cctgggaacc 2117
 cagggatttc acctccacca gtgagaccac ggggccactg tggggtgagg gaaggagcgc 2177
 ttggagtcag agctctagac cttgggtcaac tcttcacctc tgtgagagat ggtgtgtgga 2237
 ggtgcttcag aagtaaagaa ttc 2260

<210> 6
 <211> 375
 <212> PRT
 <213> human neuropeptide Y4 receptor

<400> 6

Met Asn Thr Ser His Leu Leu Ala Leu Leu Leu Pro Lys Ser Pro Gln
 1 5 10 15

Gly Glu Asn Arg Ser Lys Pro Leu Gly Thr Pro Tyr Asn Phe Ser Glu
 20 25 30

His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr
 35 40 45

Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys
 50 55 60

Val Thr Val Arg Gln Lys Glu Lys Ala Asn Val Thr Asn Leu Leu Ile
 65 70 75 80

Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Leu Cys Gln Pro
 85 90 95

Leu Thr Ala Val Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Thr
 100 105 110

Leu Cys Lys Met Ser Ala Phe Ile Gln Cys Met Ser Val Thr Val Ser
 115 120 125

Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
 130 135 140

Asn Pro Thr Gly Trp Lys Pro Ser Ile Ser Gln Ala Tyr Leu Gly Ile
 145 150 155 160

Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala
165 170 175

Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu
180 185 190

Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala
195 200 205

His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
210 215 220

Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg
225 230 235 240

Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg
245 250 255

Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val
260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu
275 280 285

Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe
290 295 300

Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
305 310 315 320

Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu
325 330 335

Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu
340 345 350

Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu
355 360 365

Ser Gly Arg Ser Asn Pro Ile
370 375

<210> 7
<211> 1423
<212> DNA

<213> human neuropeptide Y5 receptor

<220>

<221> CDS

<222> (71)..(1408)

<400> 7

gaaaggctat cggtaacaac tgacctgccca caaagttaga agaaaggatt gattcaagaa 60

agactataat atg gat tta gag ctc gag gag tat tat aac aag aca ctt 109
Met Asp Leu Glu Leu Asp Glu Tyr Tyr Asn Lys Thr Leu
1 5 10

gcc aca gag aat aat act gct gcc act cgg aat tct gat ttc cca gtc 157
Ala Thr Glu Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val
15 20 25

tgg gat gac tat aaa agc agt gta gat gac tta cag tat ttt ctg att 205
Trp Asp Asp Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile
30 35 40 45

ggg ctc tat aca ttt gta agt ctt ctt ggc ttt atg ggg aat cta ctt 253
Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu
50 55 60

att tta atg gct ctc atg aaa aag cgt aat cag aag act acg gta aac 301
Ile Leu Met Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn
65 70 75

ttc ctc ata ggc aat ctg gcc ttt tct gat atc ttg gtt gtg ctg ttt 349
Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe
80 85 90

tgc tca cct ttc aca ctg acg tct gtc ttg ctg gat cag tgg atg ttt 397
Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe
95 100 105

ggc aaa gtc atg tgc cat att atg cct ttt ctt caa tgt gtg tca gtt 445
Gly Lys Val Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val
110 115 120 125

ttg gtt tca act tta att tta ata tca att gcc att gtc agg tat cat 493
Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His
130 135 140

atg ata aaa cat ccc ata tct aat aat tta aca gca aac cat ggc tac 541
Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr
145 150 155

ttt ctg ata gct act gtc tgg aca cta ggt ttt gcc atc tgt tct ccc 589
Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro
160 165 170

ctt cca gtg ttt cac agt ctt gtg gaa ctt caa gaa aca ttt ggt tca 637
Leu Pro Val Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser
175 180 185

gca ttg ctg agc agc agg tat tta tgt gtt gag tca tgg cca tct gat 685
Ala Leu Leu Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp

190	195	200	205	
tca tac aga att gcc ttt act atc tct tta ttg cta gtt cag tat att				733
Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile	210	215	220	
ctg ccc tta gtt tgt ctt act gta agt cat aca agt gtc tgc aga agt				781
Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser	225	230	235	
ata agc tgt gga ttg tcc aac aaa gaa aac aga ctt gaa gaa aat gag				829
Ile Ser Cys Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu	240	245	250	
atg atc aac tta act ctt cat cca tcc aaa aag agt ggg cct cag gtg				877
Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val	255	260	265	
aaa ctc tct ggc agc cat aaa tgg agt tat tca ttc atc aaa aaa cac				925
Lys Leu Ser Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His	270	275	280	285
aga aga aga tat agc aag aag aca gca tgt gtg tta cct gct cca gaa				973
Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu	290	295	300	
aga cct tct caa gag aac cac tcc aga ata ctt cca gaa aac ttt ggc				1021
Arg Pro Ser Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly	305	310	315	
tct gta aga agt cag ctc tct tca tcc agt aag ttc ata cca ggg gtc				1069
Ser Val Arg Ser Gln Leu Ser Ser Ser Ser Lys Phe Ile Pro Gly Val	320	325	330	
ccc act tgc ttt gag ata aaa cct gaa gaa aat tca gat gtt cat gaa				1117
Pro Thr Cys Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu	335	340	345	
ttg aga gta aaa cgt tct gtt aca aga ata aaa aag aga tct cga agt				1165
Leu Arg Val Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser	350	355	360	365
gtt ttc tac aga ctg acc ata ctg ata tta gta ttt gct gtt agt tgg				1213
Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp	370	375	380	
atg cca cta cac ctt ttc cat gtg gta act gat ttt aat gac aat ctt				1261
Met Pro Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu	385	390	395	
att tca aat agg cat ttc aag ttg gtg tat tgc att tgt cat ttg ttg				1309
Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu	400	405	410	
ggc atg atg tcc tgt tgt ctt aat cca att cta tat ggg ttt ctt aat				1357
Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn	415	420	425	
aat ggg att aaa gct gat tta gtg tcc ctt ata cac tgt ctt cat atg				1405
Asn Gly Ile Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met				

430	435	440	445	
taa taattctcac tgttt				1423

```
<210>      8
<211>     445
<212>     PRT
<213>     human neuropeptide Y5 receptor
<400>      8
```

Met Asp Leu Glu Leu Asp Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu
1 5 10 15

Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp
20 25 30

Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser
115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
 195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu
 210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys
 225 230 235 240

Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn
 245 250 255

Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val Lys Leu Ser
 260 265 270

Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His Arg Arg Arg
 275 280 285

Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu Arg Pro Ser
 290 295 300

Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly Ser Val Arg
 305 310 315 320

Ser Gln Leu Ser Ser Ser Ser Lys Phe Ile Pro Gly Val Pro Thr Cys
 325 330 335

Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu Leu Arg Val
 340 345 350

Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr
 355 360 365

Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu
 370 375 380

His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn
 385 390 395 400

Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met
 405 410 415

Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile
 420 425 430

Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met
 435 440 445

<210> 9
 <211> 1903
 <212> DNA
 <213> human neuropeptide Y7 receptor

<220>
 <221> CDS
 <222> (369)..(1595)

<400> 9
 ctcgagatcc attgtgctct aaaggcctcc tgagtagctg ggactacagg cgcccgccac 60
 cacgcctggc taattttttt gtatttttag tagggacggc gtttactgt gttagccaga 120
 tgggtctccat ctcccgacct cgtgatccac ccacctcggc ctcccaaagt gctgggatta 180
 caggcgtgag accgcgcccg gccaatattcc tttcttagtt gcctctgccc acctcttctc 240
 ttctgcttcc atattacagg tttcctcagt tgcgaaatta ggatgttaat tatagctttt 300
 gacatacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca tgtagatcag 360
 tgactgct atg ttc atc atg aat gag aaa tgg gac aca aac tct tca gaa 410
 Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu
 1 5 10
 aac tgg cat ccc atc tgg aat gtc aat gac aca aag cat cat ctg tac 458
 Asn Trp His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr
 15 20 25 30
 tca gat att aat att acc tat gtg aac tac tat ctt cac cag cct caa 506
 Ser Asp Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln
 35 40 45
 gtg gca gca atc ttc att att tcc tac ttt ctg atc ttc ttt ttg tgc 554
 Val Ala Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys
 50 55 60
 atg atg gga aat act gtg gtt tgc ttt att gta atg agg aac aaa cat 602
 Met Met Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His
 65 70 75
 atg cac aca gtc act aat ctc ttc atc tta aac ctg gcc ata agt gat 650
 Met His Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp
 80 85 90
 tta cta gtt ggc ata ttc tgc atg cct ata aca ctg ctg gac aat att 698
 Leu Leu Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile
 95 100 105 110
 ata gca gga tgg cca ttt gga aac acg atg tgc aag atc agt gga ttg 746
 Ile Ala Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu
 115 120 125
 gtc cag gga ata tct gtc gca gct tca gtc ttt acg tta gtt gca att 794

Val Gln Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile	
130 135 140	
gct gta gat agg ttc cag tgt gtg gtc tac cct ttt aaa cca aag ctc	842
Ala Val Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu	
145 150 155	
act atc aag aca gcg ttt gtc att att atg atc atc tgg gtc cta gcc	890
Thr Ile Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala	
160 165 170	
atc acc att atg tct cca tct gca gta atg tta cat gtg caa gaa gaa	938
Ile Thr Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu	
175 180 185 190	
aaa tat tac cga gtg aga ctc aac tcc cag aat aaa acc agt cca gtc	986
Lys Tyr Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val	
195 200 205	
tac tgg tgc cgg gaa gac tgg cca aat cag gaa atg agg aag atc tac	1034
Tyr Trp Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr	
210 215 220	
acc act gtg ctg ttt gcc aac atc tac ctg gct ccc ctc tcc ctc att	1082
Thr Thr Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile	
225 230 235	
gtc atc atg tat gga agg att gga att tca ctc ttc agg gct gca gtt	1130
Val Ile Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val	
240 245 250	
cct cac aca ggc agg aag aac cag gag cag tgg cac gtg gtg tcc agg	1178
Pro His Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg	
255 260 265 270	
aag aag cag aag atc att aag atg ctc ctg att gtg gcc ctg ctt ttt	1226
Lys Lys Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe	
275 280 285	
att ctc tca tgg ctg ccc ctg tgg act cta atg atg ctc tca gac tac	1274
Ile Leu Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr	
290 295 300	
gct gac ctt tct cca aat gaa ctg cag atc atc aac atc tac atc tac	1322
Ala Asp Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr	
305 310 315	
cct ttt gca cac tgg ctg gca ttc ggc aac agc agt gtc aat ccc atc	1370
Pro Phe Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile	
320 325 330	
att tat ggt ttc ttc aac gag aat ttc cgc cgt ggt ttc caa gaa gct	1418
Ile Tyr Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala	
335 340 345 350	
ttc cag ctc cag ctc tgc caa aaa aga gca aag cct atg gaa gct tat	1466
Phe Gln Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr	
355 360 365	
acc cta aaa gct aaa agc cat gtg ctc ata aac aca tct aat cag ctt	1514

Thr Leu Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu
 370 375 380
 gtc cag gaa tct aca ttt caa aac cct cat ggg gaa acc ttg ctt tat 1562
 Val Gln Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr
 385 390 395
 agg aaa agt gct gaa aac ccc aac agg aat tag tgatggaaga attaaaagaa 1615
 Arg Lys Ser Ala Glu Asn Pro Asn Arg Asn
 400 405
 actactaaca gcagtgagat ttaaaaagag ctagtgtgat aatcctaact ctactacgca 1675
 ttatatatattt aaatccattg ctttttgtgg ctttgcactt caaattttttc aaagaatgtt 1735
 ctaaataaaaa catttactga aagccctctc tggcaaaaaa attaaaaata aacaaaaatg 1795
 gtcataagat cataaacaat cttatgttgt ataaaaatac gtagagtgac ttagacatgt 1855
 ttgcatgaat aaatatatattt ctagagaaca gttaaaaaaa aaaaaaaaa 1903

<210> 10
 <211> 408
 <212> PRT
 <213> human neuropeptide Y7 receptor

<400> 10

Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp
 1 5 10 15

His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp
 20 25 30

Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
 35 40 45

Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met
 50 55 60

Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His
 65 70 75 80

Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu
 85 90 95

Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala
 100 105 110

Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln
 115 120 125

Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val
 130 135 140

Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile
 145 150 155 160

Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr
 165 170 175

Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr
 180 185 190

Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp
 195 200 205

Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr
 210 215 220

Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile
 225 230 235 240

Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His
 245 250 255

Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys
 260 265 270

Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu
 275 280 285

Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp
 290 295 300

Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe
 305 310 315 320

Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr
 325 330 335

Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln
 340 345 350

Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu
 355 360 365

Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln
 370 375 380

Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys
 385 390 395 400

Ser Ala Glu Asn Pro Asn Arg Asn
 405

<210> 11
 <211> 1980
 <212> DNA
 <213> mouse neuropeptide Y1 receptor

<220>
 <221> CDS
 <222> (135)..(1283)

<400> 11
 aggggaatgaa gaactgagaa ttatcttggt gaatggattc aaatatatgg aataagagta 60
 tgctgaagat ttgatccgtt ttgaagaact ataactgtcc atttatctaa tcggtaacaa 120
 caaaacataa aaaa atg aac tca act ctg ttc tcc aag gtt gaa aat cac 170
 Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His
 1 5 10
 tca att cac tat aat gcc tca gag aat tct cca ctt ctg gct ttt gaa 218
 Ser Ile His Tyr Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu
 15 20 25
 aat gat gac tgc cac ctg ccc ttg gct gtg ata ttc acc ttg gct ctc 266
 Asn Asp Asp Cys His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu
 30 35 40
 gct tat ggg gcg gtg att att ctt ggc gtc tct gga aac ctg gca ttg 314
 Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu
 45 50 55 60
 atc ata atc att ctg aaa cag aag gag atg aga aat gtc acc aac att 362
 Ile Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile
 65 70 75
 ctg atc gtg aac ctc tcc ttc tca gac ttg ctc gtt gcg gtc atg tgt 410
 Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys
 80 85 90
 ctc ccg ttc act ttt gta tat aca ctg atg gac cac tgg gtc ttc ggg 458
 Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly
 95 100 105
 gag acc atg tgc aaa ctg aat ccc ttt gta cag tgt gtc tcc atc aca 506
 Glu Thr Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr
 110 115 120

gta tcc att ttc tcg ctg gtt ctc atc gct gtg gaa cgg cat cag cta Val Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu 125 130 135 140	554
atc atc aac cca aga ggg tgg aga cca aac aat aga cat gct tac ata Ile Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile 145 150 155	602
ggc att act gtc att tgg gtc ctt gca gtg gct tct tct ctg ccc ttt Gly Ile Thr Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe 160 165 170	650
gtg atc tat caa att ctg acc gac gag ccc ttc caa aat gtg tca ctt Val Ile Tyr Gln Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu 175 180 185	698
gcg gcg ttc aag gac aag tat gtg tgc ttt gac aaa ttc cca tct gac Ala Ala Phe Lys Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp 190 195 200	746
tct cac agg ctg tct tac acg act ctc ctc ctg gtg ctg cag tat ttc Ser His Arg Leu Ser Tyr Thr Thr Leu Leu Val Leu Gln Tyr Phe 205 210 215 220	794
ggc cca ctc tgc ttt ata ttc ata tgc tac ttc aag ata tac att cgc Gly Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg 225 230 235	842
ttg aaa agg aga aac aac atg atg gac aag atc cgg gac agt aag tac Leu Lys Arg Arg Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr 240 245 250	890
agg tcc agt gag acc aag cga atc aac atc atg ctg ctc tcc att gtg Arg Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val 255 260 265	938
gtc gcc ttc gcc gtc tgc tgg ctg ccc ctt acc atc ttc aac act gtg Val Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val 270 275 280	986
ttc gac tgg aac cac cag atc att gcc acc tgc aac cac aat ctg ctg Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu 285 290 295 300	1034
ttt ctg ctc tgt cac ctc acc gcc atg atc tcc acc tgc gtc aac ccc Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro 305 310 315	1082
atc ttt tat gga ttc ctg aac aaa aat ttc cag aga gac ttg cag ttc Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe 320 325 330	1130
ttc ttc aac ttt tgt gac ttc cgg tct cga gac gat gac tac gag acc Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr 335 340 345	1178
ata gcc atg tct acc atg cat acg gat gtg tcc aag acg tct ctg aag Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys 350 355 360	1226

cag gct agc cca gtc gca ttt aaa aaa atc agt atg aat gac aat gaa 1274
 Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu
 365 370 375 380

aaa gtc tga agctgctcag agcatatggt cccaggccat atctgtggaa 1323
 Lys Val

aaacaagcac agcctgccgc atgcttttctt tacctatgct ctgggggaac ggaatgaggc 1383

gcgcttggaag agcccaggac atctgtgtta aatttgactg cttttgatgg ttgccctgat 1443

tacttagaaa tctagattac tttgtaatct atctctggca acagttttga ctagatgtcc 1503

tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 1563

cgcgcgcgcgc cgcgcacgtg caaaagagaa agagagagag agaaggagag agacagacag 1623

actgcctgtc tgtctgtctg tctgtctttc tttatgtatg tgtttgaatt atgcatatga 1683

caaagagttt tacatttgtt ttgttgaggt gaatttctct gaagtaatgt catgagctca 1743

tttcaaaagc agtcaccacc tgatattctc gagaggctga attttcaaga tcagatgaga 1803

tttccgagac cccggactac cttcgttccc tgctaggcat catcttagtc tgtcacaagg 1863

gtgacagtat acaaagtcac ctttttgaat gtgcctgagt caaaagagtg tctgaagtca 1923

tttggcagca tcttttcctt ttcctctcta tttctgtaag gactcaattt cttatac 1980

<210> 12

<211> 382

<212> PRT

<213> mouse neuropeptide Y1 receptor

<400> 12

Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His Ser Ile His Tyr
 1 5 10 15

Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu Asn Asp Asp Cys
 20 25 30

His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala
 35 40 45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
 50 55 60

Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
 65 70 75 80

Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
 85 90 95

Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
 100 105 110
 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
 115 120 125
 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
 130 135 140
 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
 145 150 155 160
 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
 165 170 175
 Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
 180 185 190
 Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
 195 200 205
 Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
 210 215 220
 Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg
 225 230 235 240
 Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu
 245 250 255
 Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe Ala
 260 265 270
 Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
 275 280 285
 His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
 290 295 300
 His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
 305 310 315 320
 Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
 325 330 335

Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser
 340 345 350

Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro
 355 360 365

Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val
 370 375 380

<210> 13
 <211> 2650
 <212> DNA
 <213> mouse neuropeptide Y2 receptor

<220>
 <221> CDS
 <222> (781)..(1938)

<400> 13
 acagtcaaca cgcggaaggt ggagaaagtt gtattggtga ggcttattgg ttagaaagac 60
 cattctagtt ggtgacttcc agaccagtga gaaggcctgt ctcaaaaaac aatgtggatg 120
 gcacctgagg aatgatacct gagggttgct ttgactata gacacagatg ttcacactga 180
 accaccacaca ccccccccca cacacacacc agagggggggg ggggcttatg tgcacaagaa 240
 gtgaaagaaa aaagggctgt gtgagaatcc agctgttttg ccttatttta atctcccaaa 300
 gatcaggtgc tcagcacatg cagatgtttg cccctttggt atattttagg ctgctgtata 360
 cttacacatt tcaaacaatt aagtgggtga cactttcctt taagttaatg tgttgacttc 420
 atagcaatta taaaattgat aaactttatt gcattcattt tgcattaaaa tgggaatttat 480
 ttgatctcac tcattgtgga gctgattctc tctctaacag gaaagtgtag ttttgtcatg 540
 atcatagata ttttgaattc ctgagttcat ccatccctag ttgttaatcg acttatgtaa 600
 aggatttgct tcatcaagct tttgcaagat ctacagtgtg atgaatcaga acacagctat 660
 ccagagagct cactctaaac taaatcaatc cctttagaat ggttctctgt ttcactaact 720
 tttttttaat gtcattttta ttatagattc ttgtgttatt tacaggccaa gtgagagtga 780
 atg gtt ctg aag atg ggc ccg gta ggt gca gag gca gat gag aat caa 828
 Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln
 1 5 10 15
 act gta gaa gtg aaa gtg gag ccc tat ggg cca ggg cac act act cct 876
 Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro
 20 25 30
 aga ggt gag ttg ccc cct gat ccg gag ccg gag ctc ata gac agc acc 924

Arg	Gly	Glu	Leu	Pro	Pro	Asp	Pro	Glu	Pro	Glu	Leu	Ile	Asp	Ser	Thr		
		35					40					45					
aaa	ctg	gtc	gag	gtg	cag	gtg	atc	ctc	ata	ttg	gcc	tac	tgc	tcc	atc	972	
Lys	Leu	Val	Glu	Val	Gln	Val	Ile	Leu	Ile	Leu	Ala	Tyr	Cys	Ser	Ile		
		50				55					60						
atc	ttg	cta	ggg	gta	gtt	ggc	aac	tcc	ctg	gta	atc	cat	gtg	gta	atc	1020	
Ile	Leu	Leu	Gly	Val	Val	Gly	Asn	Ser	Leu	Val	Ile	His	Val	Val	Ile		
		65			70					75					80		
aaa	ttc	aag	agc	atg	cgc	aca	gta	acc	aac	ttt	ttt	att	gcc	aac	ctg	1068	
Lys	Phe	Lys	Ser	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Ala	Asn	Leu		
				85					90					95			
gct	gtg	gcg	gat	ctt	ttg	gtg	aac	acc	ctg	tgc	ctg	cca	ttc	act	ctt	1116	
Ala	Val	Ala	Asp	Leu	Leu	Val	Asn	Thr	Leu	Cys	Leu	Pro	Phe	Thr	Leu		
			100					105					110				
acc	tat	acc	ttg	atg	gga	gag	tgg	aaa	atg	ggt	ccg	gtc	ttg	tgc	cat	1164	
Thr	Tyr	Thr	Leu	Met	Gly	Glu	Trp	Lys	Met	Gly	Pro	Val	Leu	Cys	His		
		115					120					125					
ttg	gtg	ccc	tat	gcc	cag	ggt	ctg	gcg	gta	caa	gtg	tcc	aca	ata	act	1212	
Leu	Val	Pro	Tyr	Ala	Gln	Gly	Leu	Ala	Val	Gln	Val	Ser	Thr	Ile	Thr		
		130				135					140						
ttg	aca	gtc	att	gct	ctg	gac	cgc	cat	cgt	tgc	att	gtc	tac	cac	ctg	1260	
Leu	Thr	Val	Ile	Ala	Leu	Asp	Arg	His	Arg	Cys	Ile	Val	Tyr	His	Leu		
		145			150					155					160		
gag	agc	aag	atc	tcc	aag	cga	atc	agc	ttc	ctg	atc	att	ggc	ctg	gcc	1308	
Glu	Ser	Lys	Ile	Ser	Lys	Arg	Ile	Ser	Phe	Leu	Ile	Ile	Gly	Leu	Ala		
				165					170					175			
tgg	ggc	atc	agc	gct	ctg	ctg	gca	agt	cca	ctg	gcc	atc	ttc	cgg	gaa	1356	
Trp	Gly	Ile	Ser	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Phe	Arg	Glu		
			180					185					190				
tac	tcc	ctg	att	gag	atc	att	cct	gac	ttt	gag	att	gtg	gcc	tgt	acc	1404	
Tyr	Ser	Leu	Ile	Glu	Ile	Ile	Pro	Asp	Phe	Glu	Ile	Val	Ala	Cys	Thr		
		195					200					205					
gag	aag	tgg	cct	ggg	gaa	gag	aag	agt	gtg	tat	ggt	aca	gtc	tac	agc	1452	
Glu	Lys	Trp	Pro	Gly	Glu	Glu	Lys	Ser	Val	Tyr	Gly	Thr	Val	Tyr	Ser		
		210				215					220						
ctt	tcc	acc	ctg	ctc	atc	ctg	tac	gtt	ttg	cct	ctg	ggc	atc	ata	tct	1500	
Leu	Ser	Thr	Leu	Leu	Ile	Leu	Tyr	Val	Leu	Pro	Leu	Gly	Ile	Ile	Ser		
		225			230					235					240		
ttc	tcc	tac	acc	cgt	atc	tgg	agt	aag	ctg	agg	aac	cac	gtc	agt	cct	1548	
Phe	Ser	Tyr	Thr	Arg	Ile	Trp	Ser	Lys	Leu	Arg	Asn	His	Val	Ser	Pro		
				245					250					255			
gga	gct	gca	agt	gac	cat	tac	cat	cag	cga	agg	cac	aaa	atg	acc	aaa	1596	
Gly	Ala	Ala	Ser	Asp	His	Tyr	His	Gln	Arg	Arg	His	Lys	Met	Thr	Lys		
			260					265					270				
atg	ctg	gtg	tgc	gtg	gta	gtg	gtg	ttt	gca	gtc	agc	tgg	cta	ccc	ctc	1644	

Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu	
275 280 285	
cac gcc ttc caa ctc gct gtg gac atc gac agc cac gtc ctg gac ctg	1692
His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu	
290 295 300	
aag gag tac aaa ctc atc ttc acc gtg ttc cac att atc gcc atg tgc	1740
Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys	
305 310 315 320	
tcc acc ttt gcc aac ccc ctt ctc tat ggt tgg atg aat agc aac tac	1788
Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr	
325 330 335	
aga aaa gct ttc ctc tcg gcc ttc cgc tgt gag cag agg ttg gat gcc	1836
Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala	
340 345 350	
att cac tcg gag gtg tct atg acc ttc aag gct aaa aag aac ctg gaa	1884
Ile His Ser Glu Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu	
355 360 365	
gtc aaa aag aac aat ggc ccc act gac tct ttt tcg gag gct acc aat	1932
Val Lys Lys Asn Asn Gly Pro Thr Asp Ser Phe Ser Glu Ala Thr Asn	
370 375 380	
gtg taa ggacacaggt gtgaaagcac atgggtgaat tgtaaccagc gctgccaatc	1988
Val	
385	
tggttaggga aggttttctg gccagtgcac gcagacctcc cattgtattg actcaaaaag	2048
caacagaacc gaagccccag cagtttttatt tctggaaaac tggctggcag aaggaggtaa	2108
aaataaacag attgccatgg cacaacgttc tgattaccga tgcttggatt gtaggttgaa	2168
ttatgagtag agaaggggaag gaaaacagaa caaggagttg gcaccagcat ggttaaaagg	2228
gagaagtaag tgttatctct gagagcacag taggatctgc atcaggcaca ctgtggactc	2288
catgggctcc ctcatcactt gatgaaaagc tgctaaacaa ctgagatttc cctagggagc	2348
tacaggctct ctgttagggt gttttggttt tattgtcttt cctaagatga aaccctaatg	2408
agaatgctat aggtaaacat ggcttgctac ctaaggcggg gacttcaaga taacgtcaag	2468
agaataaaca catttgctat acgagtaatg ttttggcaat gatgggagag attcttatat	2528
aatcagtgag caattagttg ttgttcagat caaatgcact actgttgaaa gtttgttttt	2588
tagttcagaa tcaaaatctg aaattatcat actgaaaagg aatgaaaaca attgctttat	2648
tt	2650
<210> 14	
<211> 385	
<212> PRT	
<213> mouse neuropeptide Y2 receptor	

<400> 14

Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln
1 5 10 15

Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro
20 25 30

Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr
35 40 45

Lys Leu Val Glu Val Gln Val Ile Leu Ile Leu Ala Tyr Cys Ser Ile
50 55 60

Ile Leu Leu Gly Val Val Gly Asn Ser Leu Val Ile His Val Val Ile
65 70 75 80

Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu
85 90 95

Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu
100 105 110

Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His
115 120 125

Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr
130 135 140

Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu
145 150 155 160

Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala
165 170 175

Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu
180 185 190

Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr
195 200 205

Glu Lys Trp Pro Gly Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser
210 215 220

Leu Ser Thr Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser

225 230 235 240
 Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Arg Asn His Val Ser Pro
 245 250 255
 Gly Ala Ala Ser Asp His Tyr His Gln Arg Arg His Lys Met Thr Lys
 260 265 270
 Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu
 275 280 285
 His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu
 290 295 300
 Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys
 305 310 315 320
 Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr
 325 330 335
 Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala
 340 345 350
 Ile His Ser Glu Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu
 355 360 365
 Val Lys Lys Asn Asn Gly Pro Thr Asp Ser Phe Ser Glu Ala Thr Asn
 370 375 380
 Val
 385

<210> 15
 <211> 1709
 <212> DNA
 <213> mouse neuropeptide Y4 receptor

<220>
 <221> CDS
 <222> (204)..(1331)

<400> 15
 atgcctgcct cttaccttaa gccttgatg atagcctcca atgccatgag atataagcag 60
 ccaagaacct tttcccttgc ccttatcggt acctggttcc attgtagatg catggtcctt 120
 gagttccatt tgtttgtttt gcaggctgca tctctgaagt aggcccttta ctcttgagat 180

tcccggatct tctcacacct acc atg aat acc tct cat ttc ttg gcc cct ctc	233
Met Asn Thr Ser His Phe Leu Ala Pro Leu	
1 5 10	
ttc cca gga tcc cta cag ggt aag aat ggg acc aat cca ttg gat tcc	281
Phe Pro Gly Ser Leu Gln Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser	
15 20 25	
ccc tat aat ttc tct gat ggc tgc cag gat tcg gca gaa ctg ttg gcc	329
Pro Tyr Asn Phe Ser Asp Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala	
30 35 40	
ttc atc atc acc acc tac agc att gag acc atc tta ggg gtc ctg gga	377
Phe Ile Ile Thr Thr Tyr Ser Ile Glu Thr Ile Leu Gly Val Leu Gly	
45 50 55	
aac ctc tgc ttg ata ttt gtg acc aca aga caa aag gaa aag tcc aat	425
Asn Leu Cys Leu Ile Phe Val Thr Thr Arg Gln Lys Glu Lys Ser Asn	
60 65 70	
gtg acc aac cta ctc att gcc aac ctg gcc ttc tct gac ttc ctc atg	473
Val Thr Asn Leu Leu Ile Ala Asn Leu Ala Phe Ser Asp Phe Leu Met	
75 80 85 90	
tgc ctc atc tgc caa cca ctc aca gtc acc tac acc atc atg gat tac	521
Cys Leu Ile Cys Gln Pro Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr	
95 100 105	
tgg atc ttt ggt gaa gtc ctt tgc aag atg tta act ttc atc cag tgt	569
Trp Ile Phe Gly Glu Val Leu Cys Lys Met Leu Thr Phe Ile Gln Cys	
110 115 120	
atg tca gtg aca gtc tcc atc ctc tca ctg gtc ctt gtg gcc ctg gag	617
Met Ser Val Thr Val Ser Ile Leu Ser Leu Val Leu Val Ala Leu Glu	
125 130 135	
aga cac cag ctc att atc aat cca aca ggc tgg aaa ccc agt att ttc	665
Arg His Gln Leu Ile Ile Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe	
140 145 150	
cag gcc tac ctg ggg att gtg gtc atc tgg ttc atc tct tgt ttc ctt	713
Gln Ala Tyr Leu Gly Ile Val Val Ile Trp Phe Ile Ser Cys Phe Leu	
155 160 165 170	
tcc ttg ccg ttc ctg gcc aac agc acc ctg aat gac ctc ttc cac tac	761
Ser Leu Pro Phe Leu Ala Asn Ser Thr Leu Asn Asp Leu Phe His Tyr	
175 180 185	
aac cac tct aag gtt gta gag ttt ctg gaa gac aag gtc gtc tgc ttt	809
Asn His Ser Lys Val Val Glu Phe Leu Glu Asp Lys Val Val Cys Phe	
190 195 200	
gtg tcc tgg tct tca gat cac cac cgt ctc atc tat acc acc ttt ctg	857
Val Ser Trp Ser Ser Asp His His Arg Leu Ile Tyr Thr Thr Phe Leu	
205 210 215	
ctg ctc ttt cag tac tgc atc cct cta gcc ttc atc ctg gtc tgc tac	905
Leu Leu Phe Gln Tyr Cys Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr	
220 225 230	

ata cgc atc tac cag cgc ctg cag agg cag aag cat gtg ttc cat gcg	953
Ile Arg Ile Tyr Gln Arg Leu Gln Arg Gln Lys His Val Phe His Ala	
235 240 245 250	
cac gct tgc agc tca cga gcg ggg cag atg aag cgg atc aac agc atg	1001
His Ala Cys Ser Ser Arg Ala Gly Gln Met Lys Arg Ile Asn Ser Met	
255 260 265	
ctc atg aca atg gtg act gcc ttt gca gtt ctc tgg cta ccc ctg cat	1049
Leu Met Thr Met Val Thr Ala Phe Ala Val Leu Trp Leu Pro Leu His	
270 275 280	
gtg ttc aac act ctg gag gac tgg tac cag gaa gcc atc cct gct tgc	1097
Val Phe Asn Thr Leu Glu Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys	
285 290 295	
cat ggc aac ctc atc ttc ttg atg tgc cac ctg ttg gcc atg gct tcc	1145
His Gly Asn Leu Ile Phe Leu Met Cys His Leu Leu Ala Met Ala Ser	
300 305 310	
acc tgt gtc aac cct ttc atc tat ggc ttt ctc aac atc aac ttc aag	1193
Thr Cys Val Asn Pro Phe Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys	
315 320 325 330	
aag gat atc aag gct ctg gtg ctg acc tgc cat tgc agg tca cct caa	1241
Lys Asp Ile Lys Ala Leu Val Leu Thr Cys His Cys Arg Ser Pro Gln	
335 340 345	
ggg gag tct gag cat ctg ccc ctg tcc act gtt cac acg gac ctc tcc	1289
Gly Glu Ser Glu His Leu Pro Leu Ser Thr Val His Thr Asp Leu Ser	
350 355 360	
aag gga tcg atg agg atg ggt agc aag tct aac ttc ata tag	1331
Lys Gly Ser Met Arg Met Gly Ser Lys Ser Asn Phe Ile	
365 370 375	
ttgtgtctgg gcttttccct accatttttt ttgacacatc ctttcactta gttaagaaga	1391
cacattgcag gctgtgatag catcctgtca tttctggcctt ttggggccca gatagggttg	1451
caagagactt gaagccttggc attcagatgg ttttagccctt tgcttctgag agatctctga	1511
gtcaggattc tgcagatcac agagggaact ttgtggccttg agctgcaagg gtattagagt	1571
cagaagtggc tgactctcac agccactcag tacagatgcc tggcccaaaa gccttcatct	1631
atgtcctgac cattcagcta acctgccttt ggtgatgtgc ttatgttctt ccaagggatg	1691
ttgggtgttt cagtatgg	1709

<210> 16
 <211> 375
 <212> PRT
 <213> mouse neuropeptide Y4 receptor

<400> 16

Met Asn Thr Ser His Phe Leu Ala Pro Leu Phe Pro Gly Ser Leu Gln
1 5 10 15

Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser Pro Tyr Asn Phe Ser Asp
 20 25 30
 Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala Phe Ile Ile Thr Thr Tyr
 35 40 45
 Ser Ile Glu Thr Ile Leu Gly Val Leu Gly Asn Leu Cys Leu Ile Phe
 50 55 60
 Val Thr Thr Arg Gln Lys Glu Lys Ser Asn Val Thr Asn Leu Leu Ile
 65 70 75 80
 Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Ile Cys Gln Pro
 85 90 95
 Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Val
 100 105 110
 Leu Cys Lys Met Leu Thr Phe Ile Gln Cys Met Ser Val Thr Val Ser
 115 120 125
 Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
 130 135 140
 Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe Gln Ala Tyr Leu Gly Ile
 145 150 155 160
 Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala
 165 170 175
 Asn Ser Thr Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val
 180 185 190
 Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp
 195 200 205
 His His Arg Leu Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
 210 215 220
 Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr Ile Arg Ile Tyr Gln Arg
 225 230 235 240
 Leu Gln Arg Gln Lys His Val Phe His Ala His Ala Cys Ser Ser Arg
 245 250 255

Ala Gly Gln Met Lys Arg Ile Asn Ser Met Leu Met Thr Met Val Thr
 260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu
 275 280 285

Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys His Gly Asn Leu Ile Phe
 290 295 300

Leu Met Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
 305 310 315 320

Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys Lys Asp Ile Lys Ala Leu
 325 330 335

Val Leu Thr Cys His Cys Arg Ser Pro Gln Gly Glu Ser Glu His Leu
 340 345 350

Pro Leu Ser Thr Val His Thr Asp Leu Ser Lys Gly Ser Met Arg Met
 355 360 365

Gly Ser Lys Ser Asn Phe Ile
 370 375

<210> 17
 <211> 1868
 <212> DNA
 <213> mouse neuropeptide Y5 receptor

<220>
 <221> CDS
 <222> (100)..(1500)

<400> 17
 tctagatggt agttgtgttc tgagtatggt attgtcatag cgtgctattg ttcttcaagc 60
 tgctaattgga cactgtcttc ttccaagcag gactctagt atg gag gtt aaa ctt 114
 Met Glu Val Lys Leu
 1 5
 gaa gag cat ttt aac aag aca ttt gtc acg gag aac aat act gct gcc 162
 Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
 10 15 20
 agt cag aac acg gcc tcc cct gcc tgg gag gac tac aga ggc aca gag 210
 Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp Tyr Arg Gly Thr Glu
 25 30 35
 aac aat act tct gct gct cgg aac act gcc ttt cca gtc tgg gag gac 258

Asn	Asn	Thr	Ser	Ala	Ala	Arg	Asn	Thr	Ala	Phe	Pro	Val	Trp	Glu	Asp	
	40						45					50				
tat	aga	ggc	agc	gta	gac	gac	tta	caa	tac	ttc	ctg	att	ggg	ctc	tat	306
Tyr	Arg	Gly	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	
	55					60					65					
aca	ttt	gta	agt	ctt	ctt	ggt	ttt	atg	gga	aat	cta	ctt	atc	tta	atg	354
Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	
	70				75					80					85	
gct	gtt	atg	aaa	aag	cgc	aat	cag	aag	act	aca	gtg	aac	ttt	ctc	ata	402
Ala	Val	Met	Lys	Lys	Arg	Asn	Gln	Lys	Thr	Val	Asn	Phe		Leu	Ile	
				90					95					100		
ggc	aac	ctg	gcc	ttc	tcc	gac	att	ttg	gtt	gtc	ctg	ttt	tgc	tcc	cct	450
Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	
			105					110					115			
ttc	acc	ctg	acc	tct	gtc	ttg	ttg	gat	cag	tgg	atg	ttc	ggc	aaa	gcc	498
Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Ala	
		120					125					130				
atg	tgc	cat	atc	atg	cca	ttc	ctt	cag	tgt	gta	tca	gtt	ctg	gtt	tca	546
Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	
	135					140					145					
act	ctg	att	tta	ata	tcg	att	gcc	att	gtc	agg	tat	cat	atg	ata	aag	594
Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	
	150				155					160					165	
cac	cct	ata	tct	aac	aat	tta	aca	gca	aac	cat	ggc	tac	ttc	ctg	ata	642
His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	
				170					175					180		
gct	act	gtc	tgg	aca	ctg	ggc	ttt	gcc	atc	tgt	tct	ccc	ctc	cca	gtg	690
Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	
			185					190					195			
ttt	cac	agc	ctt	gtg	gaa	ctt	aag	gaa	acc	ttt	ggc	tca	gca	ttg	cta	738
Phe	His	Ser	Leu	Val	Glu	Leu	Lys	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	
		200					205					210				
agc	agc	aag	tat	ttg	tgt	gtt	gag	tca	tgg	ccc	tct	gat	tca	tac	aga	786
Ser	Ser	Lys	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	
	215					220					225					
att	gct	ttc	aca	atc	tct	tta	ttg	tta	gtt	cag	tat	atc	ctg	cct	cta	834
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	
	230				235					240					245	
gta	tgt	tta	aca	gta	agt	cat	act	agt	gtc	tgc	agg	agt	ata	agc	tgt	882
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Arg	Ser	Ile	Ser	Cys	
				250					255					260		
gga	ttg	tcc	cac	aaa	gaa	aac	aga	ctc	gaa	gaa	aat	gag	atg	atc	aac	930
Gly	Leu	Ser	His	Lys	Glu	Asn	Arg	Leu	Glu	Glu	Asn	Glu	Met	Ile	Asn	
			265					270					275			
tta	act	cta	cat	cca	tcc	aaa	aag	agt	cgg	gac	cag	gca	aaa	ccc	ccc	978

Leu Thr	Leu His	Pro Ser	Lys Lys	Ser Arg	Asp Gln	Ala Lys	Pro Pro	
280			285			290		
agc act	caa aag	tgg agc	tac tca	ttc atc	aga aag	cac cga	aga agg	1026
Ser Thr	Gln Lys	Trp Ser	Tyr Ser	Phe Ile	Arg Lys	His Arg	Arg Arg	
295			300		305			
tac agc	aag aag	acg gca	tgc gtg	tta ccc	gcc cca	gca gga	cct tcc	1074
Tyr Ser	Lys Lys	Thr Ala	Cys Val	Leu Pro	Ala Pro	Ala Gly	Pro Ser	
310		315			320		325	
cag gag	aag cac	cta acc	gtt cca	gaa aac	cca ggc	tcg gtc	cgt agc	1122
Gln Glu	Lys His	Leu Thr	Val Pro	Glu Asn	Pro Gly	Ser Val	Arg Ser	
	330			335			340	
cag ctg	tca cca	tcc agt	aag gtt	att cca	ggg gtc	ccg atc	tgc ttt	1170
Gln Leu	Ser Pro	Ser Ser	Lys Val	Ile Pro	Gly Val	Pro Ile	Cys Phe	
	345			350		355		
gag gtg	aaa cct	gaa gaa	agc tca	gat gct	cag gag	atg aga	gtc aag	1218
Glu Val	Lys Pro	Glu Glu	Ser Ser	Asp Ala	Gln Glu	Met Arg	Val Lys	
	360		365			370		
cgt tcc	ctc acg	aga ata	aag aag	aga tct	cgc agt	gtt ttc	tac aga	1266
Arg Ser	Leu Thr	Arg Ile	Lys Lys	Arg Ser	Arg Ser	Val Phe	Tyr Arg	
	375		380		385			
ctg act	ata ttg	ata tta	gtg ttc	gct gtt	agc tgg	atg cca	ctc cac	1314
Leu Thr	Ile Leu	Ile Leu	Val Phe	Ala Val	Ser Trp	Met Pro	Leu His	
390		395			400		405	
gtc ttc	cac gtg	gtg acc	gat ttc	aat gat	aac ctg	att tcc	aat agg	1362
Val Phe	His Val	Val Thr	Asp Phe	Asn Asp	Asn Leu	Ile Ser	Asn Arg	
	410			415		420		
cat ttc	aag ctg	gtg tac	tgc atc	tgt cac	ttg tta	ggc atg	atg tcc	1410
His Phe	Lys Leu	Val Tyr	Cys Ile	Cys His	Leu Leu	Gly Met	Met Ser	
	425		430			435		
tgt tgt	ctt aat	ccg atc	tta tat	gga ttc	ctt aat	aat ggt	atc aaa	1458
Cys Cys	Leu Asn	Pro Ile	Leu Tyr	Gly Phe	Leu Asn	Asn Gly	Ile Lys	
	440		445		450			
gca gac	ttg aga	gcc ctt	atc cac	tgc cta	cac atg	tca tga		1500
Ala Asp	Leu Arg	Ala Leu	Ile His	Cys Leu	His Met	Ser		
	455		460		465			
ttctctctgt	gcaccgagga	gagaagaaat	gtggagactg	cccacaatac	atctgtgcta			1560
attgatgcat	aatttacata	aacgtgttct	ggatctgaat	gccagtttgt	aatctatgta			1620
agatcattta	tgttataatg	tggttaattc	cgtcacttgt	gcagagtcaa	tgtcgatcta			1680
aggaaatttc	tgtcttgaaa	tagttacatt	accgtccatt	tcatgtcatt	ggtaataagt			1740
tgagtgtctt	cggtttcgag	taaaagttat	agctatccaa	attgttattt	tgtacaaaaa			1800
tgtgaagaagt	gaaaaagttg	ttccaaagaa	tattttaacct	cagattttaag	gaatttcctt			1860
tatctaga								1868

<210> 18
 <211> 466
 <212> PRT
 <213> mouse neuropeptide Y5 receptor

<400> 18

Met Glu Val Lys Leu Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu
 1 5 10 15

Asn Asn Thr Ala Ala Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp
 20 25 30

Tyr Arg Gly Thr Glu Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe
 35 40 45

Pro Val Trp Glu Asp Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe
 50 55 60

Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn
 65 70 75 80

Leu Leu Ile Leu Met Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr
 85 90 95

Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val
 100 105 110

Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp
 115 120 125

Met Phe Gly Lys Ala Met Cys His Ile Met Pro Phe Leu Gln Cys Val
 130 135 140

Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg
 145 150 155 160

Tyr His Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His
 165 170 175

Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys
 180 185 190

Ser Pro Leu Pro Val Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe
 195 200 205

Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro
210 215 220

Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln
225 230 235 240

Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys
245 250 255

Arg Ser Ile Ser Cys Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu
260 265 270

Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp
275 280 285

Gln Ala Lys Pro Pro Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg
290 295 300

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala
305 310 315 320

Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro
325 330 335

Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly
340 345 350

Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln
355 360 365

Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg
370 375 380

Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser
385 390 395 400

Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn
405 410 415

Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu
420 425 430

Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu
435 440 445

Asn Asn Gly Ile Lys Ala Asp Leu Arg Ala Leu Ile His Cys Leu His
 450 455 460

Met Ser
 465

<210> 19
 <211> 2281
 <212> DNA
 <213> mouse neuropeptide y6 receptor

<220>
 <221> CDS
 <222> (823)..(1938)

<400> 19
 ctgcagtcta ttggatgaag agtgtacata ttcatataat tcttaaagta ggcagaaatt 60
 aaaggggatg gaaatatata cttgtactgc cttagatagt caccaggatg ttgttacagt 120
 cttcgtttac tgcttctgaa gcctatactg atagaattaa taaaatactg agagagagag 180
 agagggacag agagagagag ggggagagag agagagagag agagagagag agagagagag 240
 agagagagag agaagagaag aaaacaaggt saagccatct gcttaactta tgtccacatt 300
 ctctcaagag cattgtccta tttgtagaat tatctatatt gttaagaatc atctccattg 360
 ttaagatttt gtgggctgga gatccagctc tgttgataaaa gtgcttgccct aacatgcatg 420
 aagtcctagg ttctattccc aaggctacat aaaaccttgt gttgtgatga atgcctgtaa 480
 tcccagtacg cagcaaggag agacaaggag gatcagaagc ttaaggacat cattttgtac 540
 atagtgagtt tgaggaaagc tgagggtaca tggaaactctc tctctctcaa aaacaaaaca 600
 aaacaaaaca aaaccttcta ctaatatctt ggattctgtt tgatttttag gatctcaaga 660
 gcatgctgac gtcatttatg tgtttccatc agatacagac agagatcata aacatttaac 720
 tcattgatta tatgttgaga gttgtccctc aagaaccaat ggccaaacat ccactgagga 780
 tacacggaag cttagaaaat ctctaattaa aatcctgaca ta atg gaa gtg ctc 834
 Met Glu Val Leu
 1
 aca aac cag cca aca cct aat aaa acc agt ggc aag agc aac aac tcg 882
 Thr Asn Gln Pro Thr Pro Asn Lys Thr Ser Gly Lys Ser Asn Asn Ser
 5 10 15 20
 gca ttt ttc tac ttt gaa tcc tgc caa ccc cct ttt cta gcc ata ctc 930
 Ala Phe Phe Tyr Phe Glu Ser Cys Gln Pro Pro Phe Leu Ala Ile Leu
 25 30 35
 ttg cta ctc ata gca tat act gtg atc cta atc atg ggc att ttt gga 978
 Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met Gly Ile Phe Gly

40										45										50										
aac	ctc	tct	ctt	atc	atc	atc	atc	ttt	aag	aaa	cag	aga	gaa	gct	caa	1026														
Asn	Leu	Ser	Leu	Ile	Ile	Ile	Ile	Phe	Lys	Lys	Gln	Arg	Glu	Ala	Gln															
		55					60					65																		
aat	gtt	acc	aac	ata	ctg	att	gcc	aac	ctg	tcc	ctc	tct	gac	atc	ttg	1074														
Asn	Val	Thr	Asn	Ile	Leu	Ile	Ala	Asn	Leu	Ser	Leu	Ser	Asp	Ile	Leu															
	70					75					80																			
gtg	tgt	gtc	atg	tgc	atc	cct	ttt	acg	gtc	atc	tac	act	ctg	atg	gac	1122														
Val	Cys	Val	Met	Cys	Ile	Pro	Phe	Thr	Val	Ile	Tyr	Thr	Leu	Met	Asp															
85					90					95					100															
cac	tgg	gta	ttt	ggg	aac	act	atg	tgt	aaa	ctc	act	tcc	tac	gtg	caa	1170														
His	Trp	Val	Phe	Gly	Asn	Thr	Met	Cys	Lys	Leu	Thr	Ser	Tyr	Val	Gln															
				105					110					115																
agt	gtc	tca	gtt	tct	gtg	tcc	ata	ttc	tcc	ctt	gtg	ttg	att	gct	att	1218														
Ser	Val	Ser	Val	Ser	Val	Ser	Ile	Phe	Ser	Leu	Val	Leu	Ile	Ala	Ile															
			120					125					130																	
gaa	cga	tat	cag	ctg	att	gtg	aac	ccc	cgt	ggc	tgg	aaa	ccc	aga	gta	1266														
Glu	Arg	Tyr	Gln	Leu	Ile	Val	Asn	Pro	Arg	Gly	Trp	Lys	Pro	Arg	Val															
		135					140					145																		
gct	cat	gcc	tat	tgg	ggg	atc	atc	ttg	att	tgg	ctc	att	tct	ctg	aca	1314														
Ala	His	Ala	Tyr	Trp	Gly	Ile	Ile	Leu	Ile	Trp	Leu	Ile	Ser	Leu	Thr															
	150					155					160																			
ttg	tct	att	ccc	tta	ttc	ctg	tcc	tac	cac	ctc	acc	aat	gag	ccc	ttt	1362														
Leu	Ser	Ile	Pro	Leu	Phe	Leu	Ser	Tyr	His	Leu	Thr	Asn	Glu	Pro	Phe															
165					170					175					180															
cat	aat	ctc	tct	ctc	cct	act	gac	atc	tac	acc	cac	cag	gta	gct	tgt	1410														
His	Asn	Leu	Ser	Leu	Pro	Thr	Asp	Ile	Tyr	Thr	His	Gln	Val	Ala	Cys															
				185					190					195																
gtg	gag	att	tgg	cct	tct	aaa	ctg	aac	caa	ctc	ctc	ttt	tct	aca	tca	1458														
Val	Glu	Ile	Trp	Pro	Ser	Lys	Leu	Asn	Gln	Leu	Leu	Phe	Ser	Thr	Ser															
			200					205					210																	
tta	ttt	atg	ctc	cag	tat	ttt	gtc	cct	ctg	ggc	ttc	att	ctt	atc	tgc	1506														
Leu	Phe	Met	Leu	Gln	Tyr	Phe	Val	Pro	Leu	Gly	Phe	Ile	Leu	Ile	Cys															
		215					220					225																		
tac	ctg	aag	atc	gtt	ctc	tgc	ctc	cga	aaa	aga	act	agg	cag	gtg	gac	1554														
Tyr	Leu	Lys	Ile	Val	Leu	Cys	Leu	Arg	Lys	Arg	Thr	Arg	Gln	Val	Asp															
		230				235					240																			
agg	aga	aag	gaa	aat	aag	agc	cgt	ctc	aat	gag	aac	aag	agg	gta	aat	1602														
Arg	Arg	Lys	Glu	Asn	Lys	Ser	Arg	Leu	Asn	Glu	Asn	Lys	Arg	Val	Asn															
245					250					255					260															
gtg	atg	ttg	att	tcc	atc	gta	gtg	act	ttt	gga	gcc	tgc	tgg	ttg	ccc	1650														
Val	Met	Leu	Ile	Ser	Ile	Val	Val	Thr	Phe	Gly	Ala	Cys	Trp	Leu	Pro															
				265					270					275																
ttg	aac	att	ttc	aat	gtc	atc	ttc	gac	tgg	tat	cat	gag	atg	ctg	atg	1698														
Leu	Asn	Ile	Phe	Asn	Val	Ile	Phe	Asp	Trp	Tyr	His	Glu	Met	Leu	Met															

280	285	290	
agc tgc cac cac gac ctg gta ttt gta gtt tgc cac ttg att gct atg			1746
Ser Cys His His Asp Leu Val Phe Val Val Cys His Leu Ile Ala Met			
295	300	305	
gtt tct act tgc ata aat cct ctc ttt tat gga ttt ctc aac aaa aac			1794
Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe Leu Asn Lys Asn			
310	315	320	
ttc cag aag gat cta atg atg ctt att cac cac tgt tgg tgt ggt gaa			1842
Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys Trp Cys Gly Glu			
325	330	335	340
cct cag gaa agt tat gaa aat att gcc atg tct act atg cac aca gat			1890
Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr Met His Thr Asp			
345	350	355	
gaa tcc aag gga tca tta aaa ctg gct cac ata cca aca ggc ata tag			1938
Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro Thr Gly Ile			
360	365	370	
aaactggtaa gcaaaatcaa agcccttctg ttatgaaaga aagagaagaa atagtatgga			1998
ataggggcaag gtgcagagga agccagactt aaacacataa tatctttggg cccagttttg			2058
ctttaagtta agcatgtcta ctccattcag ccatagaaca cacagagatt tatccctacc			2118
ctttcttttt ttccttttga agaataataa cttaaacaac ctagacatca ttactgagga			2178
agagaacaaa aatgagagag catacaagga cagcagagat gtctggggta caaaattcac			2238
gttattcgct ggaatagcta gaaagttatt agttgtgctg cag			2281

<210> 20
 <211> 371
 <212> PRT
 <213> mouse neuropeptide y6 receptor

<400> 20

Met	Glu	Val	Leu	Thr	Asn	Gln	Pro	Thr	Pro	Asn	Lys	Thr	Ser	Gly	Lys
1				5					10					15	

Ser	Asn	Asn	Ser	Ala	Phe	Phe	Tyr	Phe	Glu	Ser	Cys	Gln	Pro	Pro	Phe
			20					25					30		

Leu	Ala	Ile	Leu	Leu	Leu	Leu	Ile	Ala	Tyr	Thr	Val	Ile	Leu	Ile	Met
	35						40					45			

Gly	Ile	Phe	Gly	Asn	Leu	Ser	Leu	Ile	Ile	Ile	Ile	Phe	Lys	Lys	Gln
	50					55					60				

Arg	Glu	Ala	Gln	Asn	Val	Thr	Asn	Ile	Leu	Ile	Ala	Asn	Leu	Ser	Leu
65					70					75					80

Ser Asp Ile Leu Val Cys Val Met Cys Ile Pro Phe Thr Val Ile Tyr
85 90 95

Thr Leu Met Asp His Trp Val Phe Gly Asn Thr Met Cys Lys Leu Thr
100 105 110

Ser Tyr Val Gln Ser Val Ser Val Ser Val Ser Ile Phe Ser Leu Val
115 120 125

Leu Ile Ala Ile Glu Arg Tyr Gln Leu Ile Val Asn Pro Arg Gly Trp
130 135 140

Lys Pro Arg Val Ala His Ala Tyr Trp Gly Ile Ile Leu Ile Trp Leu
145 150 155 160

Ile Ser Leu Thr Leu Ser Ile Pro Leu Phe Leu Ser Tyr His Leu Thr
165 170 175

Asn Glu Pro Phe His Asn Leu Ser Leu Pro Thr Asp Ile Tyr Thr His
180 185 190

Gln Val Ala Cys Val Glu Ile Trp Pro Ser Lys Leu Asn Gln Leu Leu
195 200 205

Phe Ser Thr Ser Leu Phe Met Leu Gln Tyr Phe Val Pro Leu Gly Phe
210 215 220

Ile Leu Ile Cys Tyr Leu Lys Ile Val Leu Cys Leu Arg Lys Arg Thr
225 230 235 240

Arg Gln Val Asp Arg Arg Lys Glu Asn Lys Ser Arg Leu Asn Glu Asn
245 250 255

Lys Arg Val Asn Val Met Leu Ile Ser Ile Val Val Thr Phe Gly Ala
260 265 270

Cys Trp Leu Pro Leu Asn Ile Phe Asn Val Ile Phe Asp Trp Tyr His
275 280 285

Glu Met Leu Met Ser Cys His His Asp Leu Val Phe Val Val Cys His
290 295 300

Leu Ile Ala Met Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe
305 310 315 320

Leu Asn Lys Asn Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys
325 330 335

Trp Cys Gly Glu Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr
340 345 350

Met His Thr Asp Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro
355 360 365

Thr Gly Ile
370